IN THE CLAIMS

Please cancel Claims 10, 22, 35, 48, 60, 73, 86 and 98 without prejudice. Applicants will pursue the canceled claims in a related application.

Please amend Claims 11, 23, 24, 29, 36, 37, 43, 49, 52, 61, 62, 67, 74, 75, 77, 87, 90, 99, 100 and 102 as follows:

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a13 11. (amended) The method of Claim 9 wherein said second significance level is 0.06.

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a14 23. (amended) The method of Claim 21 wherein said second significance level is 0.06.

24. (amended) The method of Claim 21 wherein said first significance level (α_1) is smaller than said (α_2) and said step of indicating further comprises indicating said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

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a15 29. (amended) The method of Claim 27 wherein said threshold value is calculated using: $\tau_3 = c_3\sqrt{median(PM_i)}$ wherein said c_3 is a constant.

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a16 36. (amended) The method of Claim 34 wherein said second significance level is 0.06.

37. (amended) The method of Claim 34 wherein said first significance level (α_1) is smaller than said (α_2) and said step of indicating further comprises indicating said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

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43. (amended) The computer software product of Claim 40 wherein threshold value is calculated using: $\tau_1 = c_1\sqrt{mean(PM_i)}$ wherein said c_1 is a constant.

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49. (amended) The computer software product of Claim 47 wherein said second significance level is 0.06.

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52. (amended) The computer software product of Claim 40 wherein said testing statistic is $median((PM_i\text{-}MM_i)/(PM_i+MM_i))$.

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61. (amended) The computer software product of Claim 59 wherein said second significance level is 0.06.

62. (amended) The computer software product of Claim 59 wherein said first significance level (α_1) is smaller than said (α_2) and said computer program code for indicating further comprises computer code for indicating that said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

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67. (amended) The computer software product of Claim 66 wherein said threshold value is calculated using: $\tau_3 = c_3\sqrt{median(PM_i)}$ wherein said c_3 is a constant.

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74. (amended) The computer software product of Claim 72 wherein said second significance level is 0.06.

75. (amended) The computer software product of Claim 72 wherein said first significance level (α_1) is smaller than said (α_2) and said code for indicating further comprises code for indicating that said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

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77. (amended) A system for determining whether a transcript is present in a biological sample

comprising:

a processor; and

a memory being coupled to the processor, the memory storing a plurality of machine instructions that cause the processor to perform a plurality of logical steps when implemented by the processor, said logical steps comprising:

providing a plurality of perfect match intensity values (PM_i) and mismatch intensity values (MM_i) for the transcript, wherein each of the PM_i is paired with one of the MM_i;

calculating a p-value using one-sided Wilcoxon's signed rank test, wherein the p-value is for a null hypothesis that θ=a threshold value and an

alternative hypothesis that said $\theta >$ said threshold value, wherein said θ is a test statistic for intensity difference between said perfect match intensity values and mismatch intensity values; and

indicating whether said transcript is present based upon said p-value.

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87. (amended) The system of Claim 85 wherein said second significance level is 0.06.

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90. (amended) The computer software product of Claim 76 wherein said testing statistic is $median((PM_i-MM_i)/(PM_i+MM_i))$.

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99. (amended) The system of Claim 97 wherein said second significance level is 0.06.

100. (amended) The system of Claim 97 wherein said first significance level (α_1) is smaller than said (α_2) and said step of indicating further comprises indicating said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

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102. (amended) A system for determining whether a transcript is present in a biological sample comprising:

a processor; and

a memory being coupled to the processor, the memory storing a plurality of machine instructions that cause the processor to perform a plurality of logical steps when implemented by the processor; said logical steps comprising:

providing a plurality of perfect match intensity values (PM_i) and background intensity values (B_i) for said transcript, wherein each of said PM_i is paired with one of said B_i;

calculating a p value using one sided Wilcoxon's signed rank test, wherein said p value is for a null hypothesis that θ=a threshold value and an alternative hypothesis that said θ> said threshold value, wherein said θ is a test statistic for intensity difference between said perfect match intensity values and background intensity values; and

a27

indicating whether said transcript is present based upon said p value.

Please insert new Claim 103 as follows:

a28

103. A method for determining whether a transcript is present in a biological sample comprising:

providing a plurality of perfect match intensity values (PM_i) and mismatch intensity values (MM_i) for at least 5000 transcripts, wherein the PM_i for each of said 5000 transcripts is paired with one of the MM_i;

calculating a p-value using one-sided Wilcoxon's signed rank test, wherein the p-value is for a null hypothesis that θ=a threshold value and an alternative hypothesis that said θ> said threshold value, wherein said θ is a test statistic for intensity difference between said perfect match intensity values and mismatch intensity values; and

indicating whether said transcript is present based upon said p-value.